SEQUENCE LISTING

<110> Jaworski, Jan G. Blacklock, Brenda J. <120> FATTY ACID ELONGASE 3-KETOACYL COA SYNTHASE POLYPEPTIDES <130> 07148-108002 <150> 09/877,476 <151> 2001-06-08 <150> 60/210,326 <151> 2000-06-08 <160> 56 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1709 <212> DNA <213> Arabidopsis thaliana <220> <221> CDS <222> (1) . . . (1518) <400> 1 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 20 25 gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 35 40 caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 50 55 ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 65 gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct 288 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser

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336

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 Asn
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 Cys
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 Ala
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 Val
 Ala
 Gly
 Lys

 Ala
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 His
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					agt Ser											783	
_	_	_		_	cat His			_		_				_		831	
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						cat His 375	Tyr									1152
						cat His										1200
						cta Leu										1248
						gga Gly										1296
						rca Xaa										1344

450	tta ggg tca g Leu Gly Ser 0 455	ggc ttt aag tgt a Gly Phe Lys Cys A 460	ac agt gca gtt 1392 sn Ser Ala Val
tgg gtg gct cta aac Trp Val Ala Leu Asn 465			
cac tgc atc gac aga His Cys Ile Asp Arg 485			
tca gag act cgt gtc Ser Glu Thr Arg Val 500	Pro Asn Gly A		1521
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	392 amino ació	thaliana FAE1 (S ds from B. napus ; designated At11	
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	Leu Phe Pro I	10	15
Met Thr Ser Val Asn 1 5 Phe Phe Asn Leu Cys	Leu Phe Pro I	10 Leu Thr Ala Phe L 25	15 eu Ala Gly Lys 30 eu Ser Tyr Leu
Met Thr Ser Val Asn 1	Leu Phe Pro I Ile Asn Asp I 40	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5
Met Thr Ser Val Asn 1	Leu Phe Pro I Ile Asn Asp I 40 Thr Val Thr I 55	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe
Met Thr Ser Val Asn 1	Leu Phe Pro I Ile Asn Asp I 40 Thr Val Thr I 55 Ile Val Thr A	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P 60 Arg Pro Asn Pro V 75	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe al Tyr Leu Val 80
Met Thr Ser Val Asn 1	Leu Phe Pro II Ile Asn Asp II 40 Thr Val Thr II 55 Ile Val Thr II 70 Leu Pro Pro II Phe Tyr Gln II	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P 60 Arg Pro Asn Pro V 75 Pro His Leu Lys V	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe al Tyr Leu Val 80 al Ser Val Ser 95
Met Thr Ser Val Asn 1	Leu Phe Pro II Ile Asn Asp II 40 Thr Val Thr II 55 Ile Val Thr II 70 Leu Pro Pro II Phe Tyr Gln II	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P 60 Arg Pro Asn Pro V 75 Pro His Leu Lys V 90 Ile Arg Lys Ala A 105 Ser Trp Leu Asp P	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe al Tyr Leu Val 80 al Ser Val Ser 95 sp Thr Ser Ser 110
Met Thr Ser Val Asn 1	Leu Phe Pro II Ile Asn Asp II 40 Thr Val Thr II 55 Ile Val Thr II 70 Leu Pro Pro II Asp Asp Ser S 120	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P 60 Arg Pro Asn Pro V 75 Pro His Leu Lys V 90 Ile Arg Lys Ala A 105 Ser Trp Leu Asp P	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe al Tyr Leu Val 80 al Ser Val Ser 95 sp Thr Ser Ser 110 he Leu Arg Lys
Met Thr Ser Val Asn 1	Leu Phe Pro I Ile Asn Asp I 40 Thr Val Thr I 55 Ile Val Thr A 70 Leu Pro Pro I Phe Tyr Gln I Asp Asp Ser S 120 Gly Leu Gly A 135 Pro Arg Lys I	10 Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P 60 Arg Pro Asn Pro V 75 Pro His Leu Lys V 90 Ile Arg Lys Ala A 105 Ser Trp Leu Asp P Asp Glu Thr His G 140 Thr Phe Ala Ala A	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe al Tyr Leu Val 80 al Ser Val Ser 95 sp Thr Ser Ser 110 he Leu Arg Lys 25 ly Pro Glu Gly la Arg Glu Glu
Met Thr Ser Val Asn 1	Leu Phe Pro I Ile Asn Asp I 40 Thr Val Thr I 55 Ile Val Thr A 70 Leu Pro Pro I Phe Tyr Gln I Asp Asp Ser S 120 Gly Leu Gly A 135 Pro Arg Lys 7 150	Leu Thr Ala Phe L 25 Leu His Asn Phe L 4 Leu Leu Phe Ala P 60 Arg Pro Asn Pro V 75 Pro His Leu Lys V 90 Ile Arg Lys Ala A 105 Ser Trp Leu Asp P Asp Glu Thr His G 140 Thr Phe Ala Ala A	15 eu Ala Gly Lys 30 eu Ser Tyr Leu 5 he Thr Val Phe al Tyr Leu Val 80 al Ser Val Ser 95 sp Thr Ser Ser 110 he Leu Arg Lys 25 ly Pro Glu Gly la Arg Glu Glu 160

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Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
                            200
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
                        215
                                            220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
                    230
                                       235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
                245
                                    250
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
                                265
                                                    270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
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                                                285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
                        295
                                            300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
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                                        315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
               325
                                    330
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
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Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
                            360
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
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                                            380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
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                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
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                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
            420
                                425
                                                    430
Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
                                            460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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                                        475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
<210> 9
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<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1296 bp from B. napus elongase KCS (SEQ ID
      NO:3); designated At74
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														gga Gly		96
														tat Tyr		144
						_					_			gtt Val		192
								_			_	_		ctc Leu	_	240
														atc Ile 95		288
-	-	_	_					_	_		_	_		tct Ser		336
				-	_	_	_			_		_		aag Lys		384
														Gly 999		432
														gag Glu		480
														acc Thr 175		528
														atg Met		576
														aag Lys		624
														agt Ser		672
ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	aaa	720

Gly 225	Val	Ile	Ala	Ile	Asp 230	Leu	Ala	Lys	Asp	Leu 235	Leu	His	Val	His	Lys 240	
					gtg Val											768
					agg Arg		_	_	_			_	_		_	816
					att Ile											864
		_			cta Leu	_		_	_	_	_				_	912
					cgt Arg 310											960
				_	ttg Leu		_	_			_	_	_		_	1008
					ata Ile											1056
					ttt Phe											1104
					cat His											1152
					cat His 390											1200
					cta Leu											1248
					gga Gly											1296
					gca Ala											1344
tgg	cag	att	gct	tta	999	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	tgg	1392

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    450
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac
                                                                     1440
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
                    470
                                        475
tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca
                                                                     1488
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
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                                    490
gag act cgt gtc caa aac ggt cgg tcc taa
                                                                     1518
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                                505
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<212> PRT
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      elongase KCS (SEQ ID NO:4); designated At74
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                                25
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
                            40
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
                    70
                                        75
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
                                    90
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
                                105
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
                            120
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
                        135
                                            140
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu Thr
                    150
                                        155
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
                                    170
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
                                                     190
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
                            200
                                                205
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
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                                            220
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
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230
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Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
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Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
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                                265
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
                            280
                                                285
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
Asp Gly Lys Ser Phe Arg Cys Val Gln Gly Asp Asp Glu Asn Gly
                    310
                                        315
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
                                    330
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
                                345
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
                            360
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
                        375
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
                    390
                                        395
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
                405
                                    410
                                                         415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu
            420
                                425
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
                            440
                                                445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
                        455
                                            460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
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                                        475
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
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Glu Thr Arg Val Gln Asn Gly Arg Ser
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<210> 11
<211> 1521
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3) having mutations at positions 271, 272 and
      275; designated At114 L91C K92R
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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc qcc qqa aaa
                                                                       96
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Phe	Phe	Asn	Leu 20	Cys	Leu	Phe	Pro	Leu 25	Thr	Ala	Phe	Leu	Ala 30	Gly	Lys	
_					ata Ile		_									144
					aca Thr	_					_			_		192
-		_			atc Ile 70						_				_	240
_		_	_		ctt Leu	_		_		_	_	_	_	_		288
		_	_		ttc Phe							_				336
			_	_	gat Asp		_	_			_		_		-	384
		-	_		ggt Gly			_	_							432
_		_	_		ccc Pro 150								_	_		480
_			_		att Ile				_				_			528
					gat Asp											576
					tcg Ser				_	_	_				_	624
	_	_		_	aga Arg	_						_		_	_	672
		_		_	att Ile 230			_	_	_	_	_		_		720
aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768

Lys Asn	Thr	Tyr	Ala 245	Leu	Val	Val	Ser	Thr 250	Glu	Asn	Ile	Thr	Tyr 255	Asn	
att tac Ile Tyr	_		-				-	_	-			_	_		816
cgt gtt Arg Val			-			_				_			_	_	864
aga cgg Arg Arg 290	Ser	_				-		_	-	_	_				912
gct gac Ala Asp 305		-			_	_	-				_	_			960
ggc aaa Gly Lys															1008
cga acg Arg Thr						_	_	_		_	_			_	1056
tta ago Leu Ser															1104
ttc aaa Phe Lys 370	Asp							_	_	_				_	1152
att gad Ile Asp 385															1200
cta gag Leu Glu															1248
tca acc Ser Thr															1296
gag ttg Glu Leu															1344
gtt tgg Val Trp 450	Gln														1392
tgg gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440

Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465 470 475 cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aaq 1488 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 485 tca gag act cgt gtc cca aac ggt cgg tcc taa 1521 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser 500 <210> 12 <211> 506 <212> PRT <213> Artificial Sequence <220> <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at residues 91 and 92; designated At114 L91C K92R <400> 12 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 45 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 55 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 75 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 140 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 150 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 190 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn

250

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Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
            260
                                265
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
        275
                            280
                                                285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
                        295
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
                                        315
                    310
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
                                    330
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
            340
                                345
Leu Ser Glu Lys Leu Peu Phe Val Thr Phe Met Gly Lys Lys Leu
                            360
                                                365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
                                            380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
                    390
                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
                    470
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His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
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<210> 13
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<212> DNA
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<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3), having a mutation at position 275;
      designated At114 K92R
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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc qcc qqa aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
             20
                                 25
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													tcc Ser			1	44
													act Thr			1	92
													tat Tyr			2	40
_		_	_			_		_			_	_	agt Ser	_		2	88
													act Thr 110			3	36
Arg	Asn	Gly 115	Thr	Cys	Asp	Asp	Ser 120	Ser	Trp	Leu	Asp	Phe 125	ttg Leu	Arg	Lys	3	84
		_	_					_	-				ccc Pro			4	32
Leu 145	Leu	Gln	Val	Pro	Pro 150	Arg	Lys	Thr	Phe	Ala 155	Ala	Ala	cgt Arg	Glu	Glu 160		80
Thr	Glu	Gln	Val	Ile 165	Ile	Gly	Ala	Leu	Glu 170	Asn	Leu	Phe	aag Lys	Asn 175	Thr		28
Asn	Val	Asn	Pro 180	Lys	Asp	Ile	Gly	Ile 185	Leu	Val	Val	Asn	tca Ser 190	Ser	Met	5	576
Phe	Asn	Pro 195	Thr	Pro	Ser	Leu	Ser 200	Ala	Met	Val	Val	Asn 205	act Thr	Phe	Lys		524
Leu	Arg 210	Ser	Asn	Val	Arg	Ser 215	Phe	Asn	Leu	Gly	Gly 220	Met	ggt Gly	Cys	Ser	6	572
Ala 225	Gly	Val	Ile	Ala	Ile 230	Asp	Leu	Ala	Lys	Asp 235	Leu	Leu	cat His	Val	His 240	7	20
													act Thr			7	68

						agg Arg										816
						att Ile										864
						cta Leu 295										912
						cgt Arg										960
					_	ttg Leu		_	_			-	_	_		1008
-	_	_	_			ata Ile	_	_	_		_				_	1056
						ttt Phe										1104
		_				cat His 375			_	_	_				-	1152
	_			_		cat His	_			_	_			-		1200
		_			_	cta Leu	_	_		_	_		_		_	1248
						gga Gly										1296
						gca Ala										1344
						999 Gly 455										1392
		_				gtc Val		_	_			_			_	1440

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 490 tca gag act cgt gtc cca aac ggt cgg tcc taa 1521 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser 500 <210> 14 <211> 506 <212> PRT <213> Artificial Sequence <220> <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4), having a mutation at position 92; designated At114 K92R <400> 14 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 55 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 75 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser 90 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 150 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 170 165 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 250 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe

260 265 270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg

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280
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Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
                        295
                                            300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
                                        315
                    310
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
                                    330
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
            340
                                345
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
                            360
                                                 365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
                    390
                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                405
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
            420
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
                                            460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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                                        475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                485
                                    490
                                                         495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
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<210> 15
<211> 1521
<212> DNA
<213> Artificial Sequence
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<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3), having a mutation at position 920;
      designated At114 G307D; hypothetical
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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
             20
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
                                                                      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
         35
                             40
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		aca Thr				_		_		192
		atc Ile 70								240
		ctt Leu								288
		ttc Phe								336
		gat Asp								384
		ggt Gly								432
		ccc Pro 150								480
		att Ile								528
		gat Asp								576
		tcg Ser		 _	_	_			_	624
		aga Arg								672
		att Ile 230								720
		ctt Leu								768
		aat Asn								816

					gct Ala											864
					gag Glu											912
		_	_		ttt Phe 310		_					_	_			960
					agt Ser	_		_	_			_	_	_		1008
_	_	-	_		aac Asn		-	_	_		_	_			_	1056
					ctt Leu											1104
		_			aaa Lys				_	_	-				-	1152
					ata Ile 390											1200
		_			gcc Ala		_	_		_	_		_		_	1248
					ttt Phe											1296
					gaa Glu											1344
-		_		_	tta Leu					_	_		_	_	_	1392
					aat Asn 470											1440
					tac Tyr											1488

1521

tca gag act cgt gtc caa aac ggt cgg tcc taa

Ser Glu Thr Arg Val Gln Asn Gly Arg Ser 500 <210> 16 <211> 506 <212> PRT <213> Artificial Sequence <220> <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutation at residue 307; designated At114 G307D; hypothetical <400> 16 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser 85 90 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 105 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 140 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu 150 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 205 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 250 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 280 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly

295

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Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
                    310
                                        315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
                325
                                    330
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
            340
                                345
Leu Ser Glu Lys Leu Pee Phe Val Thr Phe Met Gly Lys Lys Leu
                            360
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
                                            380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
                    390
                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                405
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
        435
                            440
                                                 445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                                             460
                        455
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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                                    490
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
            500
<210> 17
<211> 1518
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1296 bp from B. napus elongase KCS (SEQ ID
      NO:3) having a mutation at position 917;
      designated At74 G306D; hypothetical
<221> CDS
<222> (1) ... (1515)
atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac
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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
             20
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
                                                                      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
         35
                             40
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act qtt ttc
                                                                      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
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50 ·55 60 ggt ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt 240 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val 70 gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc 288 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg 336 Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg 100 aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att 384 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile 120 caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg 432 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu 135 140 ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg 480 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu Thr 150 160 gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac 528 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn 165 gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt 576 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe 180 190 aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc 624 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu 195 cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt gcc 672 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala 210 ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat aaa 720 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys 230 235 aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac att 768 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc cgt 816 Tyr Ala Gly Asp Asn Arg Ser Met Wet Val Ser Asn Cys Leu Phe Arg 260 270 gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cqt aqa 864

Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg

	275					280			285			
				cta Leu								912
				cgt Arg 310								960
				ttg Leu								1008
				ata Ile								1056
				ttt Phe								1104
				cat His								1152
_		_		cat His 390	_		 _	_		_		1200
			_	cta Leu	_	_	_		 _		_	1248
				gga Gly								1296
				gca Ala								1344
				ggg Gly								1392
				gtc Val 470								1440
				ccg Pro								1488
				aac Asn			taa					1518

500 505

<210> 18 <211> 505 <212> PRT <213> Artificial Sequence

<220>

<223> 5' 74 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 431 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 306; designated At74 G306D; hypothetical

<400> 18 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 20 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val 70 75 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser 90 Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg 100 105 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile 120 125 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu 135 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr 150 155 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn 170 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe 180 185 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu 200 205 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala 215 220 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys 230 235 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile 250 Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg 260 265 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg 280 285 Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala 295 300 Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly 310 315 Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg

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325
                                    330
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
                                345
Ser Glu Lys Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
                            360
                                                365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
                        375
                                            380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
                    390
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
                405
                                    410
                                                         415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu
            420
                                425
                                                    430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
                            440
                                                445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
                        455
                                            460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
                    470
                                        475
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
                                    490
Glu Thr Arg Val Gln Asn Gly Arg Ser
            500
                                505
<210> 19
<211> 1521
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3) having mutations at positions 271, 272, 275
      and 920; designated At114 L91C K92R G307D;
      hypothetical
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<222> (1)...(1518)
atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac
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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
             20
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
                                                                      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
         35
                             40
                                                  45
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc
                                                                      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
     50
                         55
                                              60
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			ctc Leu													240
			tgt Cys													288
			gat Asp 100													336
			acg Thr													384
			cgt Arg													432
			gtc Val													480
acg Thr	gag Glu	caa Gln	gtt Val	atc Ile 165	att Ile	ggt Gly	gcg Ala	cta Leu	gaa Glu 170	aat Asn	cta Leu	ttc Phe	aag Lys	aac Asn 175	acc Thr	528
Asn	Val	Asn	cct Pro 180	Lys	Asp	Ile	Gly	Ile 185	Leu	Val	Val	Asn	Ser 190	Ser	Met	576
			act Thr													624
			aac Asn													672
			ata Ile													720
			tat Tyr													768
			ggt Gly 260													816
			Gly aaa													864

_			_		gag Glu		_		_	_	_	_				91	L2
_	-	-	_		ttt Phe 310	_	-					_	-			96	60
					agt Ser	_		_	-			-	-	-		100	8(
_	_	_	_		aac Asn		_	_	_		_	_			_	105	56
	_				ctt Leu			_			_		_			110)4
					aaa Lys											119	52
	_			_	ata Ile 390		-	_								120	00
					gcc Ala											124	48
					ttt Phe											12:	96
	_	-			gaa Glu	-				_	_					13	44
_				_	tta Leu					_	_		_	_	_	13	92
					aat Asn 470											14	40
	_		_	_	tac Tyr	_	_			_		_			_	14	88
			-	-	caa Gln					taa						15	21

<210> 20 <211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
NO:2) and 3' 392 amino acids from B. napus
elongase KCS (SEQ ID NO:4) having mutations at
positions 91, 92 and 307; designated At114 L91C
K92R G307D; hypothetical

<400> 20

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 20 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 125 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu 150 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 170 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 280 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 295 300 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 310 315 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330

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Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
                            360
                                                365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
                    390
                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                405
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
                                            460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
                    470
                                        475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                485
                                    490
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
            500
<210> 21
<211> 1521
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3) having mutations at positions 275 and 920;
      designated At114 K92R G307D; hypothetical
<221> CDS
<222> (1)...(1518)
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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
                                     10
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
                                 25
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
                                                                      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
         35
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc
                                                                      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
     50
                         55
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt
                                                                      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
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65					70					75					80	
_		_	_			ccg Pro		_			_	_	_	_		288
						tac Tyr										336
			_	_	_	gat Asp	_	_			_		_		_	384
		-	_			cta Leu 135		_	_							432
						cgg Arg										480
_			_			ggt Gly			_				_			528
						ata Ile										576
					_	ctc Leu			_	_	_				_	624
	_	_		_	_	agc Ser 215						_		_	_	672
_		_		_		gat Asp		_	_	_	_	_		_		720
		_		_		gtg Val		_								768
						agg Arg										816
_	_			_	_	att Ile	_				_			_	_	864
						cta Leu										912

	290					295					300					
		_	aag Lys					-				-		_		960
			gga Gly		_	_		_	_			_	_	_		1008
_	_	-	aag Lys 340				_	_	_		_	_			•	1056
	_		aaa Lys					_			_		_			1104
		-	aaa Lys						_	_	_				-	1152
			ttt Phe													1200
		_	aac Asn		_		_	_		_	_		_		_	1248
	_		cat His 420	_							_					1296
			tac Tyr													1344
_		_	att Ile	_												1392
			cta Leu													1440
	-		gac Asp	_		_	_			_		_			_	1488
			cgt Arg 500	_						taa						1521

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
NO:2) and 3' 392 amino acids from B. napus
elongase KCS (SEQ ID NO:4) having mutations at
positions 92 and 307; designated At114 K92R G307D;
hypothetical

<400> 22

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 75 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser 90 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 140 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 170 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 180 190 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 250 245 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 280 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 295 300 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 310 315 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345

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Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
        355
                            360
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
                                             380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
                    390
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                405
                                     410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
            420
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
                                             460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
                    470
                                        475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                485
                                    490
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
<210> 23
<211> 1521
<212> DNA
<213> Artificial Sequence
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<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 759 bp from B. napus elongase KCS (SEQ ID
      NO:3); designated At254
<221> CDS
<222> (1) . . . (1518)
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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac
                                                                       48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
             20
                                 25
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
                                                                      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
         35
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc
                                                                      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
     50
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt
                                                                      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65
                     70
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct
                                                                      288
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Asp	Tyr	Ser	Cys	Tyr 85	Leu	Pro	Pro	Pro	His 90	Leu	Lys	Val	Ser	Val 95	Ser	
	_	_	_		ttc Phe				_		_	_				336
			_	_	gat Asp	_	_		_		_		-		_	384
			_		ggt Gly			-		_						432
			_		ccg Pro 150		_			_			_	_		480
		_	_		atc Ile				_							528
	_			_	gag Glu									_	_	576
					tcg Ser											624
	_	_			aaa Lys	_						_		_	_	672
_		_		_	att Ile 230	_	_	_		-	_	_		-		720
					ctc Leu											768
					aat Asn											816
					gct Ala											864
_			_		gag Glu		_		_	_	_	_				912
gct	gac	ggc	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960

Ala 305	Asp	Gly	Lys	Ser	Phe 310	Arg	Cys	Val	Gln	Gln 315	Gly	Asp	Asp	Glu	Asn 320		
					_	_		_	_			_	_	gct Ala 335		1008	8
_	_	_	_					-	_		_	-		ctt Leu	_	105	6
	-							_			_		_	aaa Lys		110	4
		_							_	_	_			ctt Leu	_	115	2
	-			_			_							gat Asp		120	0
														tca Ser 415		124	8
	_			_							_			tgg Trp		129	6
														aat Asn		134	4
_		_		_						_	_		_	gca Ala		139	2
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			cgt Arg 500							taa						152	1

<210> 24

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 252 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At254

<400> 24 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 75 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser 90 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys 120 125 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 135 140 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 150 155 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr 170 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 250 Ile Tyr Ala Gly Asp Asn Arg Ser Met Wet Val Ser Asn Cys Leu Phe 260 265 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 280 285 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 295 300 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 310 315 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 345 Leu Ser Glu Lys Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 360 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 375 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val

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390
                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
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                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465
                    470
                                        475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
            500
<210> 25
<211> 1521
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1002 bp from B. napus elongase KCS (SEQ ID
      NO:3); designated At173
<221> CDS
<222> (1)...(1518)
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                 5
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gqa aaa
                                                                       96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
                                                                      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
                             40
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc
                                                                      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
                         55
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt
                                                                      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65
                     70
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct
                                                                      288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
                 85
                                      90
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca
                                                                      336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
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		100					105					110			
cgg aa Arg As		_	_	_	_	_		_		_		_		_	384
att ca Ile Gl 13	n Glu	_					_		_		_				432
ctc at Leu Il 145															480
aca ga Thr Gl		_			_	_		_				_			528
aac gt Asn Va															576
ttt aa Phe As				_				_	_	-				_	624
ctc cg Leu Ar 21	g Ser		_	_	_						_		_	-	672
gcc gg Ala Gl 225	_		_		-		-	_	_	_	_		_		720
aaa aa Lys As															768
att ta Ile Ty															816
cgt gt Arg Va			_	_		_				_			_	_	864
aga co Arg Ar 29	g Ser														912
gct ga Ala As 305															960
ggc aa Gly Ly															1008

	325	330	335
	Lys Asn Ile Ala T	cg ttg ggt ccg ttg att Thr Leu Gly Pro Leu Ile 45 350	Leu Pro
		tt acc ttc atg ggc aag al Thr Phe Met Gly Lys 365	
		ac gtc ccg gat ttc aaa yr Val Pro Asp Phe Lys 380	•
		ga ggc aga gcc gtg att ly Gly Arg Ala Val Ile 395	
		cg atc gat gta gag gca Pro Ile Asp Val Glu Ala 410	
	Arg Phe Gly Asn T	ct tca tct agc tca ata Thr Ser Ser Ser Ser Ile 25 430	Trp Tyr
		ga agg atg aag aaa ggt Bly Arg Met Lys Lys Gly 445	
		ggc ttt aag tgt aac agt Bly Phe Lys Cys Asn Ser 460	
		gct tcg aca aat agt cct Ala Ser Thr Asn Ser Pro 475	
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	gtc cma aac ggt c Val Xaa Asn Gly A 5		1521

<210> 26

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 333 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At173

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<221> VARIANT
<222> (0)...(0)
<223> Xaa = Pro or Gln
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<400> 26 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 55 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 75 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser 85 90 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 135 140 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 155 150 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 190 180 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 220 215 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 Ile Tyr Ala Gly Asp Asn Arg Ser Met Wet Val Ser Asn Cys Leu Phe 265 260 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 280 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 295 300 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 310 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 Arq Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 345 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 360 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala

375

390

Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val

380

395

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Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
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Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
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                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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<210> 27
<211> 1521
<212> DNA
<213> Artificial Sequence
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<223> 5' 528 bp from B. napus elongase KCS (SEQ ID NO:3)
      and 3' 993 bp from A. thaliana FAE1 (SEQ ID NO:1);
      designated Bn176
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ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa
                                                                       96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
                                 25
             20
ged tat egg oft acc ata gad gat oft cad cad tha tac tat too tat
                                                                      144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
         35
                             40
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt
                                                                      192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
     50
ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc
                                                                      240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65
                     70
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca aqt atc
                                                                      288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct
                                                                      336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
            100
                                 105
```

			_	_	gat Asp	_	_	_			_		_		_	384
					ggt Gly											432
_		_	_		ccc Pro 150		_						_	_		480
_			_		att Ile								_			528
	_			_	gag Glu						_			_	_	576
					tcg Ser			_	_	_	_				_	624
	_	_			aaa Lys	_						_		_	_	672
					att Ile 230											720
					ctt Leu											768
		_		_	aat Asn	_		_	_	-	_		_	_		816
					gcg Ala											864
					aag Lys											912
					ttt Phe 310											960
					tgt Cys											1008

					aat Asn										1056
					ctt Leu										1104
					aag Lys										1152
					att Ile 390										1200
					gga Gly										1248
	_			_	ttt Phe						_				1296
_		_			gag Glu	_	_		_	_	_				1344
					tta Leu										1392
				_	aat Asn 470		_	_	_	_		_			1440
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<210> 28

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 176 amino acids from B. napus elongase KCS (SEQ ID NO:4) and 3' 330 amino acids from A. thaliana FAE1 (SEQ ID NO:2); designated Bn176

<400> 28 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys 25 20 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr 40 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu 70 75 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser 105 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 125 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 150 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly 250 245 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg 280 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly 295 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser 310 315 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly 325 330 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 345 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu 360 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu 390 395 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arq 410 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr 420 425 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys

440 435 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 455 460 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln 470 475 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys 490 Ser Lys Thr His Val Gln Asn Gly Arg Ser 500 <210> 29 <211> 1521 <212> DNA <213> Artificial Sequence <220> <223> 5' 1197 bp from A. thaliana FAE1 (SEQ ID NO:1) and 3' 324 bp from B. napus elongase KCS (SEQ ID NO:3); designated At399 <221> CDS <222> (1) ... (1518) <400> 29 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 20 25 gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 35 40 caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe ggt ttg gtt etc tac atc gta acc ega ecc aat eeg gtt tat etc gtt 240 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val gac tac tcg tgt tac ctt cca ccg cat ctc aaa gtt agt gtc tct 288 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser 85 aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 110 egg aac gtg gca tgt gat gat eeg tee teg ete gat tte etg aqq aaq 384 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys 115 120 125

					ggt Gly											432
					ccg Pro 150											480
		_	_		atc Ile				-							528
					gag Glu											576
					tcg Ser			_	_	_					_	624
	_	_			aaa Lys	_						_		_	_	672
_		_		_	att Ile 230	_	_	_		_	_	_		_		720
					ctt Leu											768
		_		_	aat Asn	_		_	_	_	_		_	_		816
					gcg Ala											864
_			_		aag Lys		_		_	_	_	_				912
					ttt Phe 310											960
					tgt Cys											1008
			_		aat Asn		_		_		_	_				1056

	_	_	acc ttc gtc Thr Phe Val	_	
			gtt ccg gat Val Pro Asp 380		
		His Ala Gly	ggc aga gcc Gly Arg Ala 395		
			atc gat gta Ile Asp Val 410		r Arg
			tca tct agc Ser Ser Ser		
			agg atg aag Arg Met Lys		
			ttt aag tgt Phe Lys Cys 460		
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<210> 30 <211> 506 <212> PRT <213> Artif	icial Sequen	ce			

<220>

<223> 5' 399 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 107 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At399

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Pro or Gln

<400> 30

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Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 455 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 470 475 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 485 490 Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser 500 <210> 31 <211> 1521 <212> DNA <213> Artificial Sequence <220> <223> 5' 1197 bp from B. napus elongase KCS (SEQ ID NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID NO:1); designated Bn399 <221> CDS <222> (1) . . . (1518) <400> 31 atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac 48 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys 25 gcc tat egg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val 50 55 60 ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc 240 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu 65 70 gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile 85 tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser egg aac ggc acg tgc gat gac teg teg tgg ett gac tte ttq aqq aaq 384 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432

Ile	Gln 130	Glu	Arg	Ser	Gly	Leu 135	Gly	Asp	Glu	Thr	His 140	Gly	Pro	Glu	Gly	
			gtc Val													480
			gtt Val													528
			cct Pro 180		_									_	_	576
			act Thr													624
	_	_	aac Asn	_	_	_						_		_	_	672
			ata Ile													720
		_	tat Tyr	_				_								768
			ggt Gly 260													816
_	_		ggg Gly	_	_		_				_			_	_	864
			aag Lys									_				912
			aag Lys													960
			gga Gly													1008
			aag Lys 340													1056
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104

Leu	Ser	Glu 355	Lys	Leu	Leu	Phe	Phe 360	Val	Thr	Phe	Met	Gly 365	Lys	Lys	Leu	
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					ata Ile 390											1200
					gga Gly											1248
	_			_	ttt Phe						_					1296
_		_			gag Glu	_	_		_	_	_					1344
-		_		_	tta Leu					_	_		_		_	1392
		_		_	aat Asn 470	_	_	_	_	_		_				1440
	_		_		tat Tyr	_	_			_		_	_		_	1488
	_			_	caa Gln					taa						1521

<210> 32

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from B. napus elongase KCS (SEQ ID NO:3) and 3' 107 amino acids from A. thaliana FAE1 (SEQ ID NO:1); designated Bn399

<400> 32

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Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
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                                        75
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
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Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
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Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
                            120
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
                        135
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
                    150
                                        155
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
                165
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Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
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Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
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Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
                        215
                                            220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
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                                       235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
                                    250
                245
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
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            260
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
                            280
                                                285
        275
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
                        295
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
                    310
                                        315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
                                    330
                325
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
                                345
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
                            360
                                                365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
                                            380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
                    390
                                        395
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
                                                445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
                   470
                                        475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
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<210> 33 <211> 1524 <212> DNA <213> Artificial Sequence														
<220> <223> 1524 bp from B. napus elongase KCS (SEQ ID NO:3) having a mutation at position 920; designated Bn G307D; hypothetical <221> CDS														
<222> (1)(1518)														
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ctt ttc aac ctt tgc ttc ttt ccg tta acg Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr 20 25														
gcc tat cgg ctt acc ata gac gat ctt cac Ala Tyr Arg Leu Thr Ile Asp Asp Leu His 35 40														
ctc caa cac aac ctc ata acc atc gct cca Leu Gln His Asn Leu Ile Thr Ile Ala Pro 50 55														
ttc ggt tcg gtt ctc tac atc gca acc cgg Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg 65 70														
gtt gag tac tca tgc tac ctt cca cca acg Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr 85 90	His Cys Arg Ser Ser Ile													
tcc aag gtc atg gat atc ttt tat caa gta Ser Lys Val Met Asp Ile Phe Tyr Gln Val 100 105														
cgg aac ggc acg tgc gat gac tcg tcg tgg Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp 115 120														
att caa gaa cgt tca ggt cta ggc gat gaa Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu 130 135														
ctg ctt cag gtc cct ccc cgg aag act ttt Leu Leu Gln Val Pro Pro Arg Lys Thr Phe														

145					150					155					160	
-			_	•				cta Leu	_				_			528
								ata Ile 185								576
								gcg Ala								624
	_	_		_	_	_		aac Asn				_		_	_	672
								gca Ala								720
								agc Ser								768
								atg Met 265								816
	_			-	_		_	ctc Leu			_			_	_	864
								cac His								912
								gtg Val								960
					_	_		aag Lys	_			_	_	_		1008
								acg Thr 345								1056
	_							gtt Val			_		_			1104
								tac Tyr								1152

370 375 380 att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 390 395 cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr 420 gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 455 460 tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465 470 475 cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 490 1524 tca gag act cgt gtc caa aac ggt cgg tcc taataa Ser Glu Thr Arq Val Gln Asn Gly Arq Ser 500 <210> 34 <211> 506 <212> PRT <213> Artificial Sequence <220> <223> 506 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated Bn G307D; hypothetical <400> 34 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr 40 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu 70 75

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile 90 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser 100 105 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 150 155 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 170 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 250 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 280 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 295 300 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 310 315 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 330 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 360 365 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 375 380 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 390 395 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 410 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr 420 425 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 440 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 455 460 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 470 475 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 490 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser

<211> 1709 <212> DNA <213> Artificial Sequence <220> <223> 1709 bp from A. thaliana FAE1 (SEQ ID NO:1) having a mutation at position 275; designated At K92R; hypothetical <221> CDS · <222> (1) ... (1518) <400> 35 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 35 caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 55 ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val gac tac tcg tgt tac ctt cca cca ccg cat ctc aga gtt agt gtc tct 288 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 110 egg aac gtg gca tgt gat gat ecg tee teg ete gat tte etg agg aag 384 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys 115 att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga 432 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 130 135 ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag 480 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 145 150 aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc 528 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr 165 170

	_			_	gag Glu									_	_	576
					tcg Ser			_	_	-	_				_	624
					aaa Lys											672
_		_		_	att Ile 230	_	_	_		_	_	_		_		720
					ctt Leu											768
		_		_	aat Asn	_		_		_	_		_	_		816
					gcg Ala											864
					aag Lys											912
					ttt Phe 310											960
				_	tgt Cys	-		_								1008
			_		aat Asn		_		_		_	_				1056
tta		~	220	+++	a++	+++	ttc	act	acc	ttc	atc	qcc	aag	aaa	ctt	1104
					Leu											
Leu cta	Ser	Glu 355 gat	Lys	Phe		Phe	Phe 360 tac	Ala	Thr	Phe ccg	Val gat	Ala 365 ttc	Lys	Lys	Leu gct	1152

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg 405 410 415	1248													
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr 420 425 430	1296													
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435 440 445	1344													
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450 455 460	1392													
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln 465 470 475 480	1440													
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys 485 490 495	1488													
tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg Ser Lys Thr His Val Gln Asn Gly Arg Ser 500 505	1538													
ccaacgttta ctttgtcttt cctttctttt attggttatg aattagatgt ttactaatgt 15 tcctctcttt ttcgttataa ataaagaagt tcaattcttc ctatagtttc aaacgcgatt 16 ttaagcgttt ctatttaggt ttacatgaat ttcttttaca aaccatcttt t 17														
<210> 36 <211> 506 <212> PRT <213> Artificial Sequence														
(213) Altilitial Sequence														
<220> <223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical														
<pre><220> <223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical <400> 36 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn</pre>														
<pre><220> <223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical <400> 36 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn</pre>														
<pre><220> <223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical <400> 36 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn</pre>														
<pre><220> <223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical <400> 36 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 1</pre>														
<pre><220> <223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical <400> 36 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 1</pre>														

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 135 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 150 155 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr 170 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 185 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 200 205 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 215 220 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 230 235 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly 250 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 265 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg 280 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly 295 300 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Glu Asp Asp Glu Ser 310 315 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly 325 330 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 345 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu 360 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 375 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu 390 395 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg 405 410 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr 425 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 440 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 455 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln 470 475 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys 485 490 Ser Lys Thr His Val Gln Asn Gly Arg Ser 500

<210> 37

<211> 1521

<212> DNA

<213> Artificial Sequence

165

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and 3' 759 bp from B. napus elongase KCS (SEQ ID NO:3) and having a mutation at position 920; designated At254 G307D; hypothetical

<221> CDS <222> (1)...(1518)

<400)> 37	7														
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							ccg Pro									96
_							gat Asp 40									144
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							acc Thr									240
_		_	_				cca Pro	_				_	_	_		288
	_	_	_				caa Gln		_		_	_				336
			_	_	_	_	ccg Pro 120		_		-		_		_	384
							ggt Gly									432
							aag Lys									480
			Val				gcg Ala	Leu		Asn						528

170

175

				_							gtg Val			_	_	576
					_			_	_	_	gtt Val				_	624
											gga Gly 220					672
gct Ala 225	ggt Gly	gtt Val	att Ile	gcc Ala	att Ile 230	gat Asp	ttg Leu	gct Ala	aaa Lys	gac Asp 235	ttg Leu	ttg Leu	cat His	gtt Val	cat His 240	720
											aac Asn					768
											tca Ser					816
											aag Lys					864
											cga Arg 300					912
											gga Gly					960
						_		_	_		acc Thr	_	_	_		1008
											ccg Pro					1056
											atg Met					1104
											gat Asp 380					1152
att Ile 385	gac Asp	cat His	ttt Phe	tgt Cys	ata Ile 390	cat His	gcc Ala	gga Gly	ggc Gly	aga Arg 395	gcc Ala	gtg Val	att Ile	gat Asp	gtg Val 400	1200

cta gag aag Leu Glu Lys			la Pro I				Arg	1248		
tca acg tta Ser Thr Leu								1296		
gag ttg gca Glu Leu Ala 435		Glu Ala Ly						1344		
gtt tgg cag Val Trp Gln 450								1392		
tgg gtg gct Trp Val Ala 465	Leu Asn							1440		
cac tgc atc His Cys Ile			al Lys I				/ Lys	1488		
tca gag act Ser Glu Thr								1521		
<210> 38 <211> 506 <212> PRT <213> Artifi	icial Seq	uence								
NO:2)	<213> Artificial Sequence									

<400> 38

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 10 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 25 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 40 45 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 70 75 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser 90 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 105 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys

residue 307; designated At254 G307D; hypothetical

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120
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
                       135
                                           140
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
                   150
                                       155
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
                165
                                    170
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
                                185
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
                           200
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
                       215
                                            220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
                   230
                                       235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
               245
                                   250
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
           260
                                265
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
                            280
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
                       295
                                            300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
                   310
                                       315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
                325
                                    330
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
           340
                                345
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
                           360
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                        375
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
                                        395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                405
                                    410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                        455
                                            460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
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<210> 39

<211> 1521

<212> DNA

<213> Artificial Sequence

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and 3' 1002 bp from B. napus elongase KCS (SEQ ID NO:3) and having a mutation at position 920; designated At173 G307D

<221> CDS <222> (1) . . . (1518)

<400> 39 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 35 caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct 288 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser 85 90 aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 egg aac gtg gca tgt gat gat ecg tee teg ete gat tte etg agg aag 384 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys 115 120 att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 130 135 ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 145 150

aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc 528 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg 576

160

180 185

Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met

					tcg Ser										-	624
					aga Arg											672
		_		_	att Ile 230	_		_	_	_	_	_		_		720
		_		_	ctt Leu			-								768
		-		_	aat Asn			_	_	-			_	_		816
					gct Ala											864
_			_		gag Glu		_		_	_	_	_				912
					ttt Phe 310											960
					agt Ser											1008
					aac Asn											1056
	_				ctt Leu			_			_		_			1104
					aaa Lys											1152
					ata Ile 390											1200

		_			aac Asn			_			:	1296
 _	_		_	_	aaa Lys 440	 	_	_			:	1344
					tca Ser							1392
					aaa Lys						:	1440
					gtc Val					_	:	1488
					ggt Gly		taa					1521

<210> 40

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 333 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At173 G307D; hypothetical

<400> 40

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Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
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Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
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Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
                                185
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
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Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
                        215
                                            220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
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                                        235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
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                                    250
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
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                                265
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Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
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                            280
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
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                                            300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
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Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
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Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
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Leu Ser Glu Lys Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
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                                            380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
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Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
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Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
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Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
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Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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<223> 5' 1197 bp from B. napus elongase KCS (SEQ ID NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID NO:1) and having a mutation at nucleotide position

920; designated Bn399 G307D; hypothetical

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				ttt gcc ttc Phe Ala Phe 60		
	_	Ile Ala Th		aaa ccg gtt Lys Pro Val		
			_	tgt aga tca Cys Arg Ser	_	
		Phe Tyr G		aaa gct gat Lys Ala Asp 110		
	Thr Cys Asp			gac ttc ttg Asp Phe Leu 125		
Ile Gln Glu 130	Arg Ser Gly	Leu Gly As	sp Glu Thr	cac ggg ccc His Gly Pro 140	Glu Gly	
Leu Leu Glr 145	val Pro Pro 150	Arg Lys Th	hr Phe Ala 155	gcg gcg cgt Ala Ala Arg	Glu Glu 160	
Thr Glu Glr	val Ile Ile 165	e Gly Ala Le	eu Glu Asn 170	cta ttc aag Leu Phe Lys	Asn Thr 175	
Asn Val Ası	n Pro Lys Asp 180	o Ile Gly II	le Leu Val	gtg aac tca Val Asn Ser 190	Ser Met	
				gtt aac act Val Asn Thr		

		195				200					205				
		_	gta Val	_	_						_		_	_	672
_		-	gcc Ala		_		_	_	_	_	_		_		720
		_	gct Ala 245				_								768
			gat Asp												816
			gcc Ala												864
			tac Tyr												912
			tct Ser												960
			gtg Val 325												1008
			aaa Lys												1056
	_		ctt Leu			_	_	_	_		_				1104
			atc Ile												1152
			tgt Cys												1200
		_	tta Leu 405			_	_		_			_		_	1248
	_		aga Arg							_					1296

420 425 430 gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435 gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450 455 tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln 465 470 cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys 490 tca aag act cat gtc caa aac ggt cgg tcc taa 1521 Ser Lys Thr His Val Gln Asn Gly Arg Ser 500 <210> 42 <211> 506 <212> PRT <213> Artificial Sequence <223> 5' 399 amino acids from B. napus elongase KCS (SEQ ID NO:3) and 3' 107 amino acids from A. thaliana FAE1 (SEQ ID NO:1) having a mutation at residue 306; designated Bn399 G307D; hypothetical <400> 42 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn 5 10 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr 40 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val 55 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu 70 75 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile 90 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser 105 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 120 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 135 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 150 155

Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr

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Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
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                                            220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
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Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
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                                            300
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Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
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Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
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Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
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                                       395
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
               405
                                   410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                                425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                            440
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
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Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
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